SEQUENCE LISTING

<110> Xiao, Yonghong
Gedrich, Richard

<120> Regulation of Human transmembrane Serine Protease

<130> 02973.00035

<150> US 60/211,224
<151> 2000-06-13

<150> US 60/283,353
<151> 2001-04-13

<150> US 60/283,648
<151> 2001-04-16

<150> PCT _____ (Docket No. LIO-81-WO)
<151> 2001-06-12

<160> 36

<170> FastSEQ for Windows Version 4.0

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tgcacttcgg caccacccac atctgtggag gcacgctcat tgacgcccag tgggtgctca 180
ctnccgccca ctgcttcttc gtgnacccgg gagaaggtcc tggagggctg gaaggtgtac 240
gcgggcacca gcaacctgca ccagttgcct gaggcagcct ccattgccga gatcatcatc 300
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tgctcactgc cgcccactgc ttcttcgtga cccgggagaa ggtcctggag ggctggaagg 180
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ctcatgcggc tgtccaagcc cctgaccctg tccggtgagg gaatctgcac tccccgctct 180
cctgcccccc agccccagca ccctctgcag ccctcgcact tgtcagcatc tgtcaactca 240
tatccgggcc ccaaagcttc tgcagggcag aagtcaaaga ctcttaaaga tccttacatg 300
gaacacttct gttttataat tagggaaact gaagcccaag ggttataaat aagtttgctc 360
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atcaatagat tgaattcttt cactggtatt aactgagcac ctaggggcca aacgctatgg 480
taggcatttc acacatatga tttcatttac tcttcacaac caaccctgtg gagcaggcac 540
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tncccncgta acaccttcca gccntccagg nccttttccc gggtcacgaa gaagcagtng 420
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<210> 10
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<212> DNA
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<210> 11
<211> 1748
<212> DNA
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<210> 12
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<212> PRT
<213> Homo sapiens

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        35                  40                  45
Thr Pro Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr
    50                  55                  60
Pro Pro Gly Arg Ala Ser Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser
65                  70                  75                  80
Pro Ala Arg Ala Ser Pro Ala Leu Ala Ser Leu Ser Arg Ser Ser Ser
                85                  90                  95
Gly Arg Ser Ser Ser Ala Arg Ser Ala Ser Val Thr Thr Ser Pro Thr
            100                 105                 110
Arg Val Tyr Leu Val Arg Ala Thr Pro Val Gly Ala Val Pro Ile Arg
        115                 120                 125
Ser Ser Pro Ala Arg Ser Ala Pro Ala Thr Arg Ala Thr Arg Glu Ser
    130                 135                 140
Pro Gly Thr Ser Leu Pro Lys Phe Thr Trp Arg Glu Gly Gln Lys Gln
145                 150                 155                 160
Leu Pro Leu Ile Gly Cys Val Leu Leu Leu Ile Ala Leu Val Val Ser
                165                 170                 175
Leu Ile Ile Leu Phe Gln Phe Trp Gln Gly His Thr Gly Ile Arg Tyr
            180                 185                 190
Lys Glu Gln Arg Glu Ser Cys Pro Lys His Ala Val Arg Cys Asp Gly
        195                 200                 205
Val Val Asp Cys Lys Leu Lys Ser Asp Glu Leu Gly Cys Val Arg Phe
    210                 215                 220
Asp Trp Asp Lys Ser Leu Leu Lys Ile Tyr Ser Gly Ser Ser His Gln
225                 230                 235                 240
Trp Leu Pro Ile Cys Ser Ser Asn Trp Asn Asp Ser Tyr Ser Glu Lys
                245                 250                 255
Thr Cys Gln Gln Leu Gly Phe Glu Ser Ala His Arg Thr Thr Glu Val
            260                 265                 270
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Ala His Arg Asp Phe Ala Asn Ser Phe Ser Ile Leu Arg Tyr Asn Ser
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Thr Ile Gln Glu Ser Leu His Arg Ser Glu Cys Pro Ser Gln Arg Tyr
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Ile Ser Leu Gln Cys Ser His Cys Gly Leu Arg Ala Met Thr Gly Arg
305                 310                 315                 320
Ile Val Gly Gly Ala Leu Ala Ser Asp Ser Lys Trp Pro Trp Gln Val
                325                 330                 335
Ser Leu His Phe Gly Thr Thr His Ile Cys Gly Gly Thr Leu Ile Asp
            340                 345                 350
Ala Gln Trp Val Leu Thr Ala Ala His Cys Phe Phe Val Thr Arg Glu
        355                 360                 365
Lys Val Leu Glu Gly Trp Lys Val Tyr Ala Gly Thr Ser Asn Leu His
    370                 375                 380
Gln Leu Pro Glu Ala Ala Ser Ile Ala Glu Ile Ile Ile Asn Ser Asn
385                 390                 395                 400
Tyr Thr Asp Glu Glu Asp Asp Tyr Asp Ile Ala Leu Met Arg Leu Ser
                405                 410                 415
Lys Pro Leu Thr Leu Ser Ala His Ile His Pro Ala Cys Leu Pro Met
            420                 425                 430
His Gly Gln Thr Phe Ser Leu Asn Glu Thr Cys Trp Ile Thr Gly Phe
        435                 440                 445
Gly Lys Thr Arg Glu Thr Asp Asp Lys Thr Ser Pro Phe Leu Arg Glu
    450                 455                 460
Val Gln Val Asn Leu Ile Asp Phe Lys Lys Cys Asn Asp Tyr Leu Val
465                 470                 475                 480
Tyr Asp Ser Tyr Leu Thr Pro Arg Met Met Cys Ala Gly Asp Leu Arg
                485                 490                 495
Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
            500                 505                 510
Glu Gln Asn Asn Arg Trp Tyr Leu Ala Gly Val Thr Ser Trp Gly Thr
        515                 520                 525
Gly Cys Gly Gln Arg Asn Lys Pro Gly Val Tyr Thr Lys Val Thr Glu
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Val Leu Pro Trp Ile Tyr Ser Lys Met Glu Ser Glu Val Arg Phe Arg
545                 550                 555                 560
Lys Ser
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<212> DNA
<213> Homo sapiens

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<210> 14
<211> 492
<212> PRT
<213> Homo sapiens

<400> 14

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            20                  25                  30
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
        35                  40                  45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
    50                  55                  60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65                  70                  75                  80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
                85                  90                  95
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
            100                 105                 110
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
        115                 120                 125
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
    130                 135                 140
Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
145                 150                 155                 160
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
                165                 170                 175
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
            180                 185                 190
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
        195                 200                 205
Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
    210                 215                 220
Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
225                 230                 235                 240
Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
                245                 250                 255
Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
            260                 265                 270
Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
        275                 280                 285
Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
    290                 295                 300
Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
305                 310                 315                 320
Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn
                325                 330                 335
Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
            340                 345                 350
Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
        355                 360                 365
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Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
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385                 390                 395                 400
Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
                405                 410                 415
Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
            420                 425                 430
Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
        435                 440                 445
Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
    450                 455                 460
Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
465                 470                 475                 480
Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly
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<220>
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<220>
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<210> 17
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<210> 18
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<210> 19
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<220>
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<210> 20
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<212> PRT
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<213> Artificial Sequence

<220>
<223> BLOCKS BL00495O

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<210> 22
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
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<400> 22
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<210> 23
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<212> PRT
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<210> 24
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> BLOCKS BL01253F

<400> 24
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<210> 25
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> BLOCKS BL00495L

<400> 25
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 1   5   10   15
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<210> 26
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 26
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<210> 27
<211> 10
<212> PRT
<213> Artificial Sequence

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<400> 27
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<210> 28
<211> 834
<212> DNA
<213> Homo sapiens

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<211> 678
<212> DNA
<213> mouse

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<210> 31
<211> 577
<212> DNA
<213> mouse

<400> 31
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<210> 32
<211> 688
<212> DNA
<213> mouse

<400> 32
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<210> 33
<211> 614
<212> DNA
<213> mouse

<400> 33
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<210> 34
<211> 751
<212> DNA
<213> Homo sapiens

<400> 34
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cacgaggtgg ccacaggatt ggcaaagatt a 751

<210> 35
<211> 1230
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)...(1230)
<223> n = A,T,C or G

<400> 35
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<210> 36
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Random oligonucleotide

<400> 36
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